

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Katz, Leonard
Stassi, Diane L.
Summers Jr., Richard G.
Ruan, Xiaoan
Pereda-Lopez, Ana
Kakavas, Stephan J.
- (ii) TITLE OF THE INVENTION: NOVEL POLYKETIDE DERIVATIVES
AND RECOMBINANT METHODS FOR MAKING SAME
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Rd.
(C) CITY: Abbott Park
(D) STATE: Illinois
(E) COUNTRY: USA
(F) ZIP: 60064-3500
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 16-MAY-1979
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Dianne Casuto
(B) REGISTRATION NUMBER: P-40,943
(C) REFERENCE/DOCKET NUMBER: 4952.US.P2
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (847)-938-3137
(B) TELEFAX: (847)-938-2623
(C) TELEX:

09735056 121100

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGCCGCTGG CGGTGATGTT CACCGGACAG GGCTCCCAAC GCCCCGGCAT GGGACGACAG 60
 TTGTACGAGC ACTTCCCCGT CTTCGCCCAG GCACTGGACG AGGTCTTCGC ACTCGCCACC 120
 CCCGGACTAC GCGAGGTGAT GTTCGACCCC GACCAAGCCG AAACACTCCA ACGCACCAGC 180
 CACGCCCAGA TCGCCCTGTT CGCCTTCGAA ACCGCCCTCT ACCGACTCTG GGAATCCTGG 240
 GGCCGTGCGAC CCGACATGGT CTGCGGACAC TCGGTTCGGAG AAATCACCAG AGCCACGTC 300
 TCCGGCACCC TCACCCTCCC CGACGCCGTC CACCTCGTCA CCACACGCGG CACCCTCATG 360
 CAAAACCTGC CCCCCGGCGG CGCCATGCTC GCCGTGCGCA CCGACCCCCA CACCCTCCAA 420
 CCCCACCTCG ACAACCACCA CGACACCATC TCCATCGCCG CCATCAACGG CCCCCACGCC 480
 ACCGTCTCTCT CCGGCGACCG CACCACCTTC CACCACATCG CCACCCAACT CAACACCAAA 540
 CCCCTTCACCA CCACCCTCAA CACCCTCACC CACCACCCCC CACACACACC CCTCATCAGC 600
 ATGCTCACCG CCACACCCAC CCACCCCGAC ACCACCCACT GGACCCAGCA CATCACCGCA 660
 CCCGTCCGCT ACACCGACAC CCTCCACCAC CTCCACCACC ACGGCATCAC CACCTACCTC 720
 GAAATCGGCC CCGACACCAC CCTCACCGCC CTCGCCCCGA CCACCTCCC CACCACCACC 780
 CACCTCATCC CCACCACCCG CCGCAACCAC AACGAAGTCC GCAGCACGAA CGAGGCGTTG 840
 GGCAGGGTGT TCAGCGTGGG CCACTCGGTG GACTGGCGGG CCCTCACTCC GACCGGGAGG 900
 CGTACCTCCC TGCCGACGTA CCCCCT 925

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTAGGACGG CAGTCCTGCT CACCGGGCAG GGTTCCCAGC GTCAGGGCAT GGGGCGCGAA 60
 CTGTACGACC GGTCAACCGGT GTTCGCCGCC TCGTTCGACG CGATCTGCGC TCAACTCGAC 120
 GGGCAACTGC CTCGTCCCCT CAAGGACGTT CTCTTCGCCC CCGAGGGGTC GGAGGACGCC 180
 GCGCTCATCG ACCGTACGGT GTTCACACAG GCGGCTCTGT TCGCCGTGGA GACCTCCCTG 240
 TTCCGGCTGT TCGAGGCCCA CGGCCTCGTC CCGCACTACC TCATCGGCCA CTCCATCGGC 300
 GAAGTGACCG CGGCCACCT GGCCGGGGTC CTCGATCTGG CCGACGCGTG CGTCCTGGTC 360
 GCCCACCGCG GCCGCTGAT GCAGTCGGCC CGGGCCGGCG GCGCGATGGC CGCGGTCCAG 420
 GCGAGCGAGG ACGAGGTACG CGAGGCCCTC GCGACCTTCG ACGATGCGGT TGCCGTGGCC 480
 GGAGTCAACG GCGCGACGC CACCGTCGTC TCCGGCGACG AGGACGCGGT CGAGCGGCTG 540
 GTCGCGCGCT GCGCGAGCA GGGCAGGCGG ACGAAGCGGC TGCCGGTCAG CCACGCTTC 600
 CACTCGCCGC ACATGGACGG GATCGTCGAC GAGTTCGTCA CCGCCGTCTC CGGGCTCACC 660
 TTCCGCTCCC CGACGATCCC GGTCGTCTCC AACGTCACCG GGACCCTCGC CACCGTCGAC 720
 CAGCTGACCT CGCCCGCGTA CTGGGCACGC CACATCCGCG AGGCCGTGCG CTTGCGCCGAC 780
 GGGGTGCGGT ACCTGGAGGG CGAGGGCGTC ACCGAATGGC TGGAGCTCGG GCCCGACGGC 840

GTTCTCGTCG CCCTGGTCGA GGA CTGCCTG GCGAAGGAGG CGGGATCGCT CGCGTCCGCC 900
 CTGCGCAAGG GGGCGAGCGA GCCCCACACC GTGGGCGCGG CCATGGCCCCG CGCGGTGCTG 960
 CGCGGATCCG GCCCCGACTG GGCGGCGGTG TTCCCCGGCG CACGGCGGGT CGACCTTCCG 1020
 ACGTATGCAT 1030

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATCTACACST CSGGCACSAC SGGCAAGCCS AAGGG

35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTSAAGGCSG GCGGCGCSTA CGTSCCSATC GACCC

35

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCGAATTCC TAGGCTGGCG GTGATGTTCA

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCCGGATCCA TGCATACGTC GGCAGGGAGG TAC

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTCGAATTC GCTGGTCGCG GTGCACCT

28

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACGGATCCG GCCCTAGGCT GCGCCCGGCT CG

32

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGGGATCCT ATGCATTCCA GCGCGAGCGC

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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GAGAAGCTTG GCGCGACTTG CCCGCT

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTTTTAAGC TTGGTACCTG CTCACCGGCA ACACCG

36

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTTTTGGAT CCCTGCAGCC TAGGGTCGGA GGCAGTCCG GT

42

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTTTTTCTGC AGTATGCATT CCAGGGCAAG CGGTTCT

37

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTTTTGAAT TCACGCGTTG CCCGCGGCGT AGGCGC

36

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCGAATTC CCTAGGACGG CAGTCCTGCT CACC

34

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCGGATCC ATGCATACGT CGGAAGGTCG ACCCG

35

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCGAAGAAT TCCCTAGGGT TGCCTTCCTG TTCGAC

36

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCGAAAAGC TTATGCATAG ACCGGCAGAT CCACCG

36

(2) INFORMATION FOR SEQ ID NO:19:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGGTSAAGTC SAACATCGG

19

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCRATCTCRC CCTGCGARTG

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGAGAGGAA CCAACGCGCA CGTGATCGTC GAAGAGGCAC CAGC

44

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAGAGAGGAT CCGACCTAGG CGCGGAGGTC ACCGGCGCGA CGGCG

45

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAGAGACCTA GGAAGCCGGT GTTCGTGTTT CCCGGCCAGG GCT

43

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAGAGAGGAT CCGAGGCCGG CCGTGCGCCC GGACCGAAGA CCGCCTC

47

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGAGAATTC CCTAGGGTCG CTTTCGTCTT TCCCGGGCAG G

41

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTGAGATCTT ATGCATACGA GGGAAGCGGC ACCCTGC

37

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTGAGATCTT ATGCATACGA GGAAGCGGC ACCCTGC

37

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTGAGATCTT ATGCATACGA GGAAGCGGC ACCCTGC

37

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1010 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCCGACCGTG	TCGTGTTCTG	GTTCCCCGGC	CAGGGCTCGC	AGTGGGCCGG	AATGGCCGAG	60
GGGCTGCTGG	AGCGGTCCGG	CGCGTTCGG	AGTGCGGCCG	ACTCGTGCGA	CGCCGCGCTG	120
CGGCCGTACC	TCGGCTGGTC	GGTGCTGAGC	GTGCTGCGCG	GGGAACCGGA	CGCGCCCTCG	180
CTCGACCGGG	TCGACGTCGT	GCAGCCGGTG	CTGTTACAGA	TGATGGTCTC	GCTCGCGGCG	240
GTCTGGCGTG	CGCTGGGGGT	GGAACCGGCG	GCGGTCGTCG	GGCACTCGCA	GGGTGAGATC	300
GCCGCTGCCC	ATGTCGCCGG	TGCGCTGTCT	CTGGACGACT	CGGCCCGGAT	CGTCGCCCTG	360
CGCAGTCGGG	CGTGGCTCGG	ACTGGCGGGC	AAGGGCGGCA	TGGTGGCGGT	GCCGATGCCG	420
GCGGAGGAGC	TGCGGCCCGG	GCTGGTGACG	TGGGGGGACC	GTCTGGCCGT	CGCCGCCGTC	480
AACAGCCCCG	GTTCTTGCGC	GCTCGCAGGC	GACCCGGAGG	CGCTGGCCGA	ACTGGTGGCG	540
CTGCTGACCG	GTGAGGGGGT	GCACGCCCGG	CCGATCCCCG	GCGTCGACAC	GGCGGGCCAC	600
TCGCCGCAGG	TGGACGCGTT	GCGGGCTCAT	CTGCTGGAGG	TGCTGGCCCC	GGTCGCCCCC	660
CGACCGGCCG	ACATCCCGTT	CTACTCGACG	GTGACCGGCG	GGCTGCTGGA	CGGCACCGAG	720
CTGGACGCGA	CGTACTGGTA	CCGCAACATG	CGCGAGCCCC	TCGAGTTCGA	GCGGGCCACA	780
CGGGCGCTGA	TCGCCGACGG	GCACGACGTC	TTCCTGGAGA	CGAGCCCGCA	TCCCATGCTG	840
GCCGTGGCGC	TGGAGCAGAC	GGTCACCGAC	GCCGGCACC	ACGCGGCGGT	GCTCGGGACC	900
CTGCGCCGCC	GCCACGGCGG	TCCTCGCGCG	CTGGCCCTGG	CCGTCTGCCG	CGCCTTCGCG	960
AGGCGGTCTT	CGGTCCGGGC	GCACGGCCCC	TGGAGTTGCC	CACCTATCCG		1010

(2) INFORMATION FOR SEQ ID NO:30:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGCGCGCCTG CCTTCGTCTT TCCCGGGCAG GCGCCCCAGT GGGCCGGACT GGGAGCGCGG 60
 CTCCTCGCGG ACTCCCCCGT CTTCCGCGCC AGGGCCGAGG CATGCGCGCG GCGCTGGAG 120
 CCTCACCTCG ACTGGTCGGT CCTCGACGTG CTGGCCGGCG CCCCAGGCAC CCCTCCCATC 180
 GACCGGGCCG ACGTGGTGCA GCCGGTGCTG TTCACCACGA TGGTCTCGCT GGCCGCCCTC 240
 TGGGAGGCCC ACGGGGTGCG GCCGGCCGCG GTCGTGGGCC ACTCCCAGGG CGAGGTGGCC 300
 GCGGCCTGCG TGGCCGGTGC CCTGTCGCTG GACGACGCTG CCCTGGTGAT CGCCGGACGC 360
 AGCAGGGCTGT GGGGCGGCT GGCCGGGAAC GCGGGGATGC TCGCGGTGAT GGCTCCGGCC 420
 GAGCGGATCC GTGAGCTGCT CGAACCATGG CCGCAGCGGA TTTCGGTGGC GCGGGTCAAT 480
 GGCCCCGCCT CGGTACCGT CTCCGGTGAC GCGCTCGCGC TGGAGGAGTT CCGCGCGCGG 540
 CTCTCCGCGG AGGGGGTGCT GCGCTGGCCG CTGCCGGGCG TCGACTTCGC CGGCCACTCG 600
 CCGCAGGTGG AGGAGTTCCG CGCTGAGCTC CTGGACCTGC TCTCCGGCGT ACGGCCGGCT 660
 CCTTCGCGGA TACCTTTCTT CTCCACCGTG ACGGCGGGTC CTGCGGCGG CGACCAGCTG 720
 GACGGGGCGT ACTGGTACCG CAACACGCGC GAACCCGTGG AGTTCGACGC CACGGTCCGG 780
 GCGCTGCTGC GTGCGGGCCA TCACACGTTT ATCGAGGTCG GTCCGCATCC GCTGCTCAAC 840
 GCCGCGATCG ACGAGATCGC AGCGGACGAG GGGGTAGCGG CCACGGCCCT GCATACGCTC 900
 CAGCGGGGCG CTGGCGGCCT TGACCGCGTG CGCAACGCGG TGGGCGCCGC TTTCGCGCAC 960
 GGTGTCCGGG TCGACTGGAA CGCCCTGTTC GAGGGCACCG GTGCGCGCAG GGTGCCGCTT 1020
 CCTCGTACG CCTTC 1035

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Pro Leu Ala Val Met Phe Thr Gly Gln Gly Ser Gln Arg Pro Gly
 1 5 10 15
 Met Gly Arg Gln Leu Tyr Glu His Phe Pro Val Phe Ala Gln Ala Leu
 20 25 30
 Asp Glu Val Phe Ala Leu Ala Thr Pro Gly Leu Arg Glu Val Met Phe
 35 40 45
 Asp Pro Asp Gln Ala Glu Thr Leu Gln Arg Thr Asp His Ala Gln Ile
 50 55 60
 Ala Leu Phe Ala Phe Glu Thr Ala Leu Tyr Arg Leu Trp Glu Ser Trp
 65 70 75 80
 Gly Leu Arg Pro Asp Met Val Cys Gly His Ser Val Gly Glu Ile Thr
 85 90 95
 Ala Ala His Val Ser Gly Thr Leu Thr Leu Pro Asp Ala Val His Leu

100 105 110
 Val Thr Thr Arg Gly Thr Leu Met Gln Asn Leu Pro Pro Gly Gly Ala
 115 120 125
 Met Leu Ala Val Ala Thr Asp Pro His Thr Leu Gln Pro His Leu Asp
 130 135 140
 Asn His His Asp Thr Ile Ser Ile Ala Ala Ile Asn Gly Pro His Ala
 145 150 155 160
 Thr Val Leu Ser Gly Asp Arg Thr Thr Leu His His Ile Ala Thr Gln
 165 170 175
 Leu Asn Thr Lys Thr Asn Trp Leu Asn Val Ser His Ala Phe His Ser
 180 185 190
 Pro Leu Met Gln Pro Ile Leu Gln Pro Phe Thr Thr Thr Leu Asn Thr
 195 200 205
 Leu Thr His His Pro Pro His Thr Pro Leu Ile Ser Met Leu Thr Ala
 210 215 220
 Thr Pro Thr His Pro Asp Thr Thr His Trp Thr Gln His Ile Thr Ala
 225 230 235 240
 Pro Val Arg Tyr Thr Asp Thr Leu His His Leu His His His Gly Ile
 245 250 255
 Thr Thr Tyr Leu Glu Ile Gly Pro Asp Thr Thr Leu Thr Ala Leu Ala
 260 265 270
 Arg Thr Thr Leu Pro Thr Thr Thr His Leu Ile Pro Thr Thr Arg Arg
 275 280 285
 Asn His Asn Glu Val Arg Ser Thr Asn Glu Ala Leu Gly Arg Val Phe
 290 295 300
 Ser Val Gly His Ser Val Asp Trp Arg Ala Leu Thr Pro Thr Gly Arg
 305 310 315 320
 Arg Thr Ser Leu Pro Thr Tyr Pro
 325

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Pro Arg Thr Ala Val Leu Leu Thr Gly Gln Gly Ser Gln Arg Gln Gly
 1 5 10 15
 Met Gly Arg Glu Leu Tyr Asp Arg Ser Pro Val Phe Ala Ala Ser Phe
 20 25 30
 Asp Ala Ile Cys Ala Gln Leu Asp Gly Gln Leu Pro Arg Pro Leu Lys
 35 40 45
 Asp Val Leu Phe Ala Pro Glu Gly Ser Glu Asp Ala Ala Leu Ile Asp
 50 55 60
 Arg Thr Val Phe Thr Gln Ala Ala Leu Phe Ala Val Glu Thr Ser Leu
 65 70 75 80
 Phe Arg Leu Phe Glu Ala His Gly Leu Val Pro Asp Tyr Leu Ile Gly

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85 90 95
 His Ser Ile Gly Glu Val Thr Ala Ala His Leu Ala Gly Val Leu Asp
 100 105 110
 Leu Ala Asp Ala Cys Val Leu Val Ala His Arg Gly Arg Leu Met Gln
 115 120 125
 Ser Ala Arg Ala Gly Gly Ala Met Ala Ala Val Gln Ala Ser Glu Asp
 130 135 140
 Glu Val Arg Glu Ala Leu Ala Thr Phe Asp Asp Ala Val Ala Val Ala
 145 150 155 160
 Gly Val Asn Gly Pro Asn Ala Thr Val Val Ser Gly Asp Glu Asp Ala
 165 170 175
 Val Glu Arg Leu Val Ala Arg Trp Arg Glu Gln Gly Arg Arg Thr Lys
 180 185 190
 Arg Leu Pro Val Ser His Ala Phe His Ser Pro His Met Asp Gly Ile
 195 200 205
 Val Asp Glu Phe Val Thr Ala Val Ser Gly Leu Thr Phe Arg Ser Pro
 210 215 220
 Thr Ile Pro Val Val Ser Asn Val Thr Gly Thr Leu Ala Thr Val Asp
 225 230 235 240
 Gln Leu Thr Ser Pro Ala Tyr Trp Ala Arg His Ile Arg Glu Ala Val
 245 250 255
 Arg Phe Ala Asp Gly Val Arg Tyr Leu Glu Gly Glu Gly Val Thr Glu
 260 265 270
 Trp Leu Glu Leu Gly Pro Asp Gly Val Leu Val Ala Leu Val Glu Asp
 275 280 285
 Cys Leu Ala Lys Glu Ala Gly Ser Leu Ala Ser Ala Leu Arg Lys Gly
 290 295 300
 Ala Ser Glu Pro His Thr Val Gly Ala Ala Met Ala Arg Ala Val Leu
 305 310 315 320
 Arg Gly Ser Gly Pro Asp Trp Ala Ala Val Phe Pro Gly Ala Arg Arg
 325 330 335
 Val Asp Leu Pro Thr Tyr Ala
 340

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Asp Arg Val Val Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Ala
 1 5 10 15
 Gly Met Ala Glu Gly Leu Leu Glu Arg Ser Gly Ala Phe Arg Ser Ala
 20 25 30
 Ala Asp Ser Cys Asp Ala Ala Leu Arg Pro Tyr Leu Gly Trp Ser Val
 35 40 45
 Leu Ser Val Leu Arg Gly Glu Pro Asp Ala Pro Ser Leu Asp Arg Val

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50 55 60
 Asp Val Val Gln Pro Val Leu Phe Thr Met Met Val Ser Leu Ala Ala
 65 70 75 80
 Val Trp Arg Ala Leu Gly Val Glu Pro Ala Ala Val Val Gly His Ser
 85 90 95
 Gln Gly Glu Ile Ala Ala Ala His Val Ala Gly Ala Leu Ser Leu Asp
 100 105 110
 Asp Ser Ala Arg Ile Val Ala Leu Arg Ser Arg Ala Trp Leu Gly Leu
 115 120 125
 Ala Gly Lys Gly Gly Met Val Ala Val Pro Met Pro Ala Glu Glu Leu
 130 135 140
 Arg Pro Arg Leu Val Thr Trp Gly Asp Arg Leu Ala Val Ala Ala Val
 145 150 155 160
 Asn Ser Pro Gly Ser Cys Ala Val Ala Gly Asp Pro Glu Ala Leu Ala
 165 170 175
 Glu Leu Val Ala Leu Leu Thr Gly Glu Gly Val His Ala Arg Pro Ile
 180 185 190
 Pro Gly Val Asp Thr Ala Gly His Ser Pro Gln Val Asp Ala Leu Arg
 195 200 205
 Ala His Leu Leu Glu Val Leu Ala Pro Val Ala Pro Arg Pro Ala Asp
 210 215 220
 Ile Pro Phe Tyr Ser Thr Val Thr Gly Gly Leu Leu Asp Gly Thr Glu
 225 230 235 240
 Leu Asp Ala Thr Tyr Trp Tyr Arg Asn Met Arg Glu Pro Val Glu Phe
 245 250 255
 Glu Arg Ala Thr Arg Ala Leu Ile Ala Asp Gly His Asp Val Phe Leu
 260 265 270
 Glu Thr Ser Pro His Pro Met Leu Ala Val Ala Leu Glu Gln Thr Val
 275 280 285
 Thr Asp Ala Gly Thr Asp Ala Ala Val Leu Gly Thr Leu Arg Arg Arg
 290 295 300
 His Gly Gly Pro Arg Ala Leu Ala Leu Ala Val Cys Arg Ala Phe Ala
 305 310 315 320
 His Gly Val Glu Val Asp Pro Glu Ala Val Phe Gly Pro Gly Ala Arg
 325 330 335
 Pro Val Glu Leu Pro Thr Tyr Pro
 340

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Ala Pro Ala Phe Val Phe Pro Gly Gln Gly Ala Gln Trp Ala Gly
 1 5 10 15
 Leu Gly Ala Arg Leu Leu Ala Asp Ser Pro Val Phe Arg Ala Arg Ala

20 25 30
 Glu Ala Cys Ala Arg Ala Leu Glu Pro His Leu Asp Trp Ser Val Leu
 35 40 45
 Asp Val Leu Ala Gly Ala Pro Gly Thr Pro Pro Ile Asp Arg Ala Asp
 50 55 60
 Val Val Gln Pro Val Leu Phe Thr Thr Met Val Ser Leu Ala Ala Leu
 65 70 75 80
 Trp Glu Ala His Gly Val Arg Pro Ala Ala Val Val Gly His Ser Gln
 85 90 95
 Gly Glu Val Ala Ala Ala Cys Val Ala Gly Ala Leu Ser Leu Asp Asp
 100 105 110
 Ala Ala Leu Val Ile Ala Gly Arg Ser Arg Leu Trp Gly Arg Leu Ala
 115 120 125
 Gly Asn Gly Gly Met Leu Ala Val Met Ala Pro Ala Glu Arg Ile Arg
 130 135 140
 Glu Leu Leu Glu Pro Trp Arg Gln Arg Ile Ser Val Ala Ala Val Asn
 145 150 155 160
 Gly Pro Ala Ser Val Thr Val Ser Gly Asp Ala Leu Ala Leu Glu Glu
 165 170 175
 Phe Gly Ala Arg Leu Ser Ala Glu Gly Val Leu Arg Trp Pro Leu Pro
 180 185 190
 Gly Val Asp Phe Ala Gly His Ser Pro Gln Val Glu Glu Phe Arg Ala
 195 200 205
 Glu Leu Asp Leu Leu Ser Gly Val Arg Pro Ala Pro Ser Arg Ile
 210 215 220
 Pro Phe Phe Ser Thr Val Thr Ala Gly Pro Cys Gly Gly Asp Gln Leu
 225 230 235 240
 Asp Gly Ala Tyr Trp Tyr Arg Asn Thr Arg Glu Pro Val Glu Phe Asp
 245 250 255
 Ala Thr Val Arg Ala Leu Leu Arg Ala Gly His His Thr Phe Ile Glu
 260 265 270
 Val Gly Pro His Pro Leu Leu Asn Ala Ala Ile Asp Glu Ile Ala Ala
 275 280 285
 Asp Glu Gly Val Ala Ala Thr Ala Leu His Thr Leu Gln Arg Gly Ala
 290 295 300
 Gly Gly Leu Asp Arg Val Arg Asn Ala Val Gly Ala Ala Phe Ala His
 305 310 315 320
 Gly Val Arg Val Asp Trp Asn Ala Leu Phe Glu Gly Thr Gly Ala Arg
 325 330 335
 Arg Val Pro Leu Pro Ser Tyr Ala Phe
 340 345

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